



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/806,413

Source: Per/09

Date Processed by STIC: 4/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/806,413

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES) Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/806,413

DATE: 04/16/2001
TIME: 09:26:39

Input Set : A:\Q63731 sequence listing.txt
Output Set: N:\CRF3\04122001\I806413.raw

Does Not Comply
Corrected Diskette Needed

pp 1-2

3 <110> APPLICANT: Amano Enzyme, Inc.
5 <120> TITLE OF INVENTION: NOVEL ENZYME COMPOSITION AND PRODUCTION METHOD AND USE THEREOF
7 <130> FILE REFERENCE: Q63731
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/806,413
C--> 9 <141> CURRENT FILING DATE: 2001-03-30
9 <150> PRIOR APPLICATION NUMBER: JP 10-294675
10 <151> PRIOR FILING DATE: 1998-09-30
12 <160> NUMBER OF SEQ ID NOS: 16
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 22
18 <212> TYPE: PRT
19 <213> ORGANISM: Aspergillus fumigatus
21 <400> SEQUENCE: 1
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24 1 5 10 15
26 Leu Ser Ser Ile Ala Ala
27 20
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 22
31 <212> TYPE: PRT
32 <213> ORGANISM: Aspergillus fumigatus
34 <400> SEQUENCE: 2
36 Leu Met Thr Pro Ala Gly Ala Asn Phe Ala Leu Met Arg His Thr Ile
37 1 5 10 15
39 Gly Ala Ser Asp Leu Ser
40 20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 28
44 <212> TYPE: DNA
C--> 45 <213> ORGANISM: Artificial *see item 11 on Env Summary Sheet*
47 <220> FEATURE:
48 <223> OTHER INFORMATION: synthetic DNA
50 <220> FEATURE:
51 <221> NAME/KEY: misc_feature
52 <223> OTHER INFORMATION: "n" may be a c, g or t
55 <400> SEQUENCE: 3
56 acgaattcaa ywsngcnggn aaytayaa 28
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 28
61 <212> TYPE: DNA
C--> 62 <213> ORGANISM: Artificial *item 11*
64 <220> FEATURE:
65 <223> OTHER INFORMATION: synthetic DNA
67 <220> FEATURE:
68 <221> NAME/KEY: misc_feature
69 <223> OTHER INFORMATION: "n" may be a c, g or t

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72 <400> SEQUENCE: 4
 OK 73 cggaattcta ytgysnaay wsnngcngg 28
 76 <210> SEQ ID NO: 5
 77 <211> LENGTH: 28
 78 <212> TYPE: DNA
 C--> 79 <213> ORGANISM: Artificial *dem 11*
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: synthetic DNA
 84 <220> FEATURE:
 85 <221> NAME/KEY: misc_feature
 86 <223> OTHER INFORMATION: "n" may be a c, g or t
 89 <400> SEQUENCE: 5
 OK 90 tcaagcttgc raarttngcn ccngcngg 28
 93 <210> SEQ ID NO: 6
 94 <211> LENGTH: 28
 95 <212> TYPE: DNA
 C--> 96 <213> ORGANISM: Artificial
 98 <220> FEATURE:
 99 <223> OTHER INFORMATION: synthetic DNA
 101 <220> FEATURE:
 102 <221> NAME/KEY: misc_feature
 103 <223> OTHER INFORMATION: "n" may be a c, g or t
 106 <400> SEQUENCE: 6
 OK 107 agaagcttgc nccdatngtr tgnckcat 28
 110 <210> SEQ ID NO: 7
 111 <211> LENGTH: 1401
 112 <212> TYPE: DNA
 113 <213> ORGANISM: Aspergillus fumigatus
 115 <400> SEQUENCE: 7
 116 gccgcctctg cttcggttta ctgttccaac tcggccggca actacaagct gtcctccatc 60
 118 gcagctccgg ttcaaggggc cggaaacccc ggctcgggaat cgacctggca attgaccgtt 120
 120 gacgacactt cgtccggtca caaacagacg atagtgtggg tcggtgctgc tgtcactgat 180
 122 gccacggtca cctcgttcaa cactttgtcc gcctccgtgc tgcaagactt gctcaataaa 240
 124 ctgatgacac ctgccggggc gaactttgct ttgatgacac atactattgg ggcttcggat 300
 126 ctgtccggtg acccagccta cacgtacgat gacaatggtg ggaaagcgga tccgtcactg 360
 128 tcgggattca acctggggga ccgcggaacg gctatggcca agatgttggc aacaatgaag 420
 130 tctctgcagc ccaacctcaa gatcctcgcc tctccctgga gtgcaccagg atggatgaag 480
 132 ctgaacgggg tccttgatgg caatacgaac aacaacaact tgaacgatgg atacctaac 540
 134 agtgggggaa ccggtatgat ggggtatgcc agtcaattcg cgcagtactt tgtcaagtac 600
 136 attcaggcct ataagaatct cgggtgtcac gtcgacgca ttaccatcca gaacgagccg 660
 138 ctgttcagct cagcgggcta tcccaccatg tatgtctacg attatgagtc ggcacagctg 720
 140 atccagaact acatcgcccc cgctcttgcc agcgcggggc tagatacggg aatctgggct 780
 142 tatgaccaca acacagatgt ccgctcgtac cccagactg tccttaacca ggccggtcag 840
 144 tacgtcaagt cgggtggcctg gcaactgctac gctcccaacg tcgactggac cgtgctcagc 900
 146 cagttccaca acacaaaccc tggagtgaag caatatatga ccgagtgtcg gactccagca 960
 148 tctggcgcat gcgcatcagg gccggacttc accatgggtc ccctgcagaa ctgggcctcg 1020
 150 ggagtggcag catggactct gggaaccaac gctcaggatg gtccgcatct gtccactggc 1080
 152 ggctgcgcga catgtcaagg cttggtgacc atcaacaacg gaggatacac gctcaacacc 1140
 154 gcatactaca tgatggcgca attcagcaag ttcattgcgc ctggtgcgat tgtgctcaat 1200

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\Q63731 sequence listing.txt

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156 ggcagtggca gctacacgta ctctggcgga ggcggtatcc agtccgtggc ttccttgaat 1260
158 cccgatggaa cccgcactgt ggttattgaa aacacttttg gcaatgatgt ctatgtgact 1320
160 gtcactatga agagcgggca gaagtggagt gggaacgccc ctagccaatc cgtgactacc 1380
162 tgggttcttc catctgcttg a                                     1401
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166 <211> LENGTH: 466
167 <212> TYPE: PRT
168 <213> ORGANISM: Aspergillus fumigatus
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173 1 5 10 15
175 Leu Ser Ser Ile Ala Ala Pro Val Gln Gly Ala Gly Asn Pro Gly Ser
176 20 25 30
178 Glu Ser Thr Trp Gln Leu Thr Val Asp Asp Thr Ser Ser Gly His Lys
179 35 40 45
181 Gln Thr Ile Val Gly Phe Gly Ala Ala Val Thr Asp Ala Thr Val Thr
182 50 55 60
184 Ser Phe Asn Thr Leu Ser Ala Ser Val Leu Gln Asp Leu Leu Asn Lys
185 65 70 75 80
187 Leu Met Thr Pro Ala Gly Ala Asn Phe Ala Leu Met Arg His Thr Ile
188 85 90 95
190 Gly Ala Ser Asp Leu Ser Gly Asp Pro Ala Tyr Thr Tyr Asp Asp Asn
191 100 105 110
193 Gly Gly Lys Ala Asp Pro Ser Leu Ser Gly Phe Asn Leu Gly Asp Arg
194 115 120 125
196 Gly Thr Ala Met Ala Lys Met Leu Ala Thr Met Lys Ser Leu Gln Pro
197 130 135 140
199 Asn Leu Lys Ile Leu Gly Ser Pro Trp Ser Ala Pro Gly Trp Met Lys
200 145 150 155 160
202 Leu Asn Gly Val Leu Asp Gly Asn Thr Asn Asn Asn Leu Asn Asp
203 165 170 175
205 Gly Tyr Leu Thr Ser Gly Gly Thr Gly Ser Thr Gly Tyr Ala Ser Gln
206 180 185 190
208 Phe Ala Gln Tyr Phe Val Lys Tyr Ile Gln Ala Tyr Lys Asn Leu Gly
209 195 200 205
211 Ala His Val Asp Ala Ile Thr Ile Gln Asn Glu Pro Leu Phe Ser Ser
212 210 215 220
214 Ala Gly Tyr Pro Thr Met Tyr Val Tyr Asp Tyr Glu Ser Ala Gln Leu
215 225 230 235 240
217 Ile Gln Asn Tyr Ile Gly Pro Ala Leu Ala Ser Ala Gly Leu Asp Thr
218 245 250 255
220 Glu Ile Trp Ala Tyr Asp His Asn Thr Asp Val Pro Ser Tyr Pro Gln
221 260 265 270
223 Thr Val Leu Asn Gln Ala Gly Gln Tyr Val Lys Ser Val Ala Trp His
224 275 280 285
226 Cys Tyr Ala Pro Asn Val Asp Trp Thr Val Leu Ser Gln Phe His Asn
227 290 295 300
229 Thr Asn Pro Gly Val Lys Gln Tyr Met Thr Glu Cys Trp Thr Pro Ala
230 305 310 315 320

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232 Ser Gly Ala Trp His Gln Ala Ala Asp Phe Thr Met Gly Pro Leu Gln
233           325           330           335
235 Asn Trp Ala Ser Gly Val Ala Ala Trp Thr Leu Gly Thr Asn Ala Gln
236           340           345           350
238 Asp Gly Pro His Leu Ser Thr Gly Gly Cys Ala Thr Cys Gln Gly Leu
239           355           360           365
241 Val Thr Ile Asn Asn Gly Gly Tyr Thr Leu Asn Thr Ala Tyr Tyr Met
242           370           375           380
244 Met Ala Gln Phe Ser Lys Phe Met Pro Pro Gly Ala Ile Val Leu Asn
245 385           390           395           400
247 Gly Ser Gly Ser Tyr Thr Tyr Ser Gly Gly Gly Gly Ile Gln Ser Val
248           405           410           415
250 Ala Ser Leu Asn Pro Asp Gly Thr Arg Thr Val Val Ile Glu Asn Thr
251           420           425           430
253 Phe Gly Asn Asp Val Tyr Val Thr Val Thr Met Lys Ser Gly Gln Lys
254           435           440           445
256 Trp Ser Gly Asn Ala Pro Ser Gln Ser Val Thr Thr Trp Val Leu Pro
257           450           455           460
259 Ser Ala
260 465
262 <210> SEQ ID NO: 9
263 <211> LENGTH: 1647
264 <212> TYPE: DNA
265 <213> ORGANISM: Aspergillus fumigatus
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (54)..(1517)
271 <220> FEATURE:
272 <221> NAME/KEY: mat_peptide
273 <222> LOCATION: (120)..()
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277                                     Met
280 cgt ata tct gtc ggt gct ctg ctt ggc ttg aca gcc ctg agt cat gcc           104
281 Arg Ile Ser Val Gly Ala Leu Leu Gly Leu Thr Ala Leu Ser His Ala
282 -20 -15 -10
284 aca aca gag aaa cga gcc gcc tot gct tcg gct tac tgt tcc aac tcg           152
285 Thr Thr Glu Lys Arg Ala Ala Ser Ala Ser Ala Tyr Cys Ser Asn Ser
286 -5 -1 1 5 10
288 gcc ggc aac tac aag ctg tcc tcc atc gca gct ccg gtt caa ggg gcc           200
289 Ala Gly Asn Tyr Lys Leu Ser Ser Ile Ala Ala Pro Val Gln Gly Ala
290 15 20 25
292 gga aac ccc ggc tcg gaa tcg acc tgg caa ttg acc gtt gac gac act           248
293 Gly Asn Pro Gly Ser Glu Ser Thr Trp Gln Leu Thr Val Asp Asp Thr
294 30 35 40
296 tcg tcc ggt cac aaa cag acg ata gtt ggg ttc ggt gct gtc act           296
297 Ser Ser Gly His Lys Gln Thr Ile Val Gly Phe Gly Ala Ala Val Thr
298 45 50 55
300 gat gcc acg gtc acc tcg ttc aac act ttg tcc gcc tcc gtg ctg caa           344

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Input Set : A:\Q63731 sequence listing.txt

Output Set: N:\CRF3\04122001\I806413.raw

301	Asp	Ala	Thr	Val	Thr	Ser	Phe	Asn	Thr	Leu	Ser	Ala	Ser	Val	Leu	Gln	
302	60					65				70					75		
304	gac	ttg	ctc	aat	aaa	ctg	atg	aca	cct	gcc	ggg	gcg	aac	ttt	gct	ttg	392
305	Asp	Leu	Leu	Asn	Lys	Leu	Met	Thr	Pro	Ala	Gly	Ala	Asn	Phe	Ala	Leu	
306				80						85					90		
308	atg	cga	cat	act	att	ggg	gct	tcg	gat	ctg	tcc	ggt	gac	cca	gcc	tac	440
309	Met	Arg	His	Thr	Ile	Gly	Ala	Ser	Asp	Leu	Ser	Gly	Asp	Pro	Ala	Tyr	
310				95					100					105			
312	acg	tac	gat	gac	aat	ggg	ggg	aaa	gcg	gat	ccg	tca	ctg	tcg	gga	ttc	488
313	Thr	Tyr	Asp	Asp	Asn	Gly	Gly	Lys	Ala	Asp	Pro	Ser	Leu	Ser	Gly	Phe	
314			110					115					120				
316	aac	ctg	ggg	gac	cg	gga	acg	gct	atg	gcc	aag	atg	ttg	gca	aca	atg	536
317	Asn	Leu	Gly	Asp	Arg	Gly	Thr	Ala	Met	Ala	Lys	Met	Leu	Ala	Thr	Met	
318		125					130					135					
320	aag	tct	ctg	cag	ccc	aac	ctc	aag	atc	ctc	ggc	tct	ccc	tgg	agt	gca	584
321	Lys	Ser	Leu	Gln	Pro	Asn	Leu	Lys	Ile	Leu	Gly	Ser	Pro	Trp	Ser	Ala	
322	140					145					150				155		
324	cca	gga	tgg	atg	aag	ctg	aac	ggg	gtc	ctt	gat	ggc	aat	acg	aac	aac	632
325	Pro	Gly	Trp	Met	Lys	Leu	Asn	Gly	Val	Leu	Asp	Gly	Asn	Thr	Asn	Asn	
326				160						165					170		
328	aac	aac	ttg	aac	gat	gga	tac	cta	acc	agt	ggg	gga	acc	ggt	agt	acg	680
329	Asn	Asn	Leu	Asn	Asp	Gly	Tyr	Leu	Thr	Ser	Gly	Gly	Thr	Gly	Ser	Thr	
330				175						180				185			
332	ggg	tat	gcc	agt	caa	ttc	gcg	cag	tac	ttt	gtc	aag	tac	att	cag	gcc	728
333	Gly	Tyr	Ala	Ser	Gln	Phe	Ala	Gln	Tyr	Phe	Val	Lys	Tyr	Ile	Gln	Ala	
334			190					195					200				
336	tat	aag	aat	ctc	ggt	gct	cac	gtc	gac	gcg	att	acc	atc	cag	aac	gag	776
337	Tyr	Lys	Asn	Leu	Gly	Ala	His	Val	Asp	Ala	Ile	Thr	Ile	Gln	Asn	Glu	
338		205				210					215						
340	ccg	ctg	ttc	agc	tca	gcg	ggc	tat	ccc	acc	atg	tat	gtc	tac	gat	tat	824
341	Pro	Leu	Phe	Ser	Ser	Ala	Gly	Tyr	Pro	Thr	Met	Tyr	Val	Tyr	Asp	Tyr	
342	220					225					230				235		
344	gag	tcg	gca	cag	ctg	atc	cag	aac	tac	atc	ggc	ccc	gct	ctt	gcc	agc	872
345	Glu	Ser	Ala	Gln	Leu	Ile	Gln	Asn	Tyr	Ile	Gly	Pro	Ala	Leu	Ala	Ser	
346				240						245				250			
348	gcg	ggg	cta	gat	acg	gaa	atc	tgg	gct	tat	gac	cac	aac	aca	gat	gtc	920
349	Ala	Gly	Leu	Asp	Thr	Glu	Ile	Trp	Ala	Tyr	Asp	His	Asn	Thr	Asp	Val	
350				255					260					265			
352	ccg	tcg	tac	ccc	cag	act	gtc	ctt	aac	cag	gcc	ggt	cag	tac	gtc	aag	968
353	Pro	Ser	Tyr	Pro	Gln	Thr	Val	Leu	Asn	Gln	Ala	Gly	Gln	Tyr	Val	Lys	
354			270					275					280				
356	tcg	gtg	gcc	tgg	cac	tgc	tac	gct	ccc	aac	gtc	gac	tgg	acc	gtg	ctc	1016
357	Ser	Val	Ala	Trp	His	Cys	Tyr	Ala	Pro	Asn	Val	Asp	Trp	Thr	Val	Leu	
358		285					290					295					
360	agc	cag	ttc	cac	aac	aca	aac	cct	gga	gtg	aag	caa	tat	atg	acc	gag	1064
361	Ser	Gln	Phe	His	Asn	Thr	Asn	Pro	Gly	Val	Lys	Gln	Tyr	Met	Thr	Glu	
362	300					305					310				315		
364	tgc	tgg	act	cca	gca	tct	ggc	gca	tgg	cat	cag	gcg	gcg	gac	ttc	acc	1112
365	Cys	Trp	Thr	Pro	Ala	Ser	Gly	Ala	Trp	His	Gln	Ala	Ala	Asp	Phe	Thr	

VERIFICATION SUMMARY

DATE: 04/16/2001

PATENT APPLICATION: US/09/806,413

TIME: 09:26:40

Input Set : A:\Q63731 sequence listing.txt

Output Set: N:\CRF3\04122001\I806413.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:45 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:56 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:62 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:73 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:79 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:96 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:543 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:555 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:567 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:579 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:591 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:603 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16